Multimodal MRI Fusion to Guide Glioblastoma Treatment Planning

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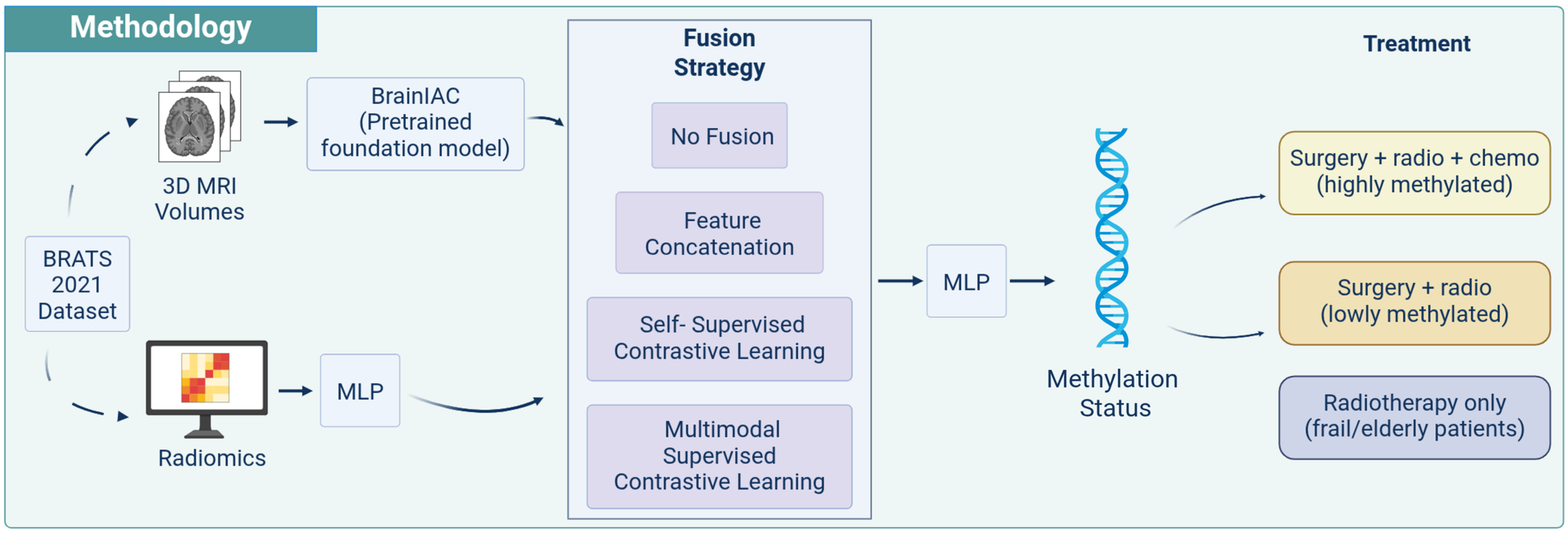
BACKGROUND

Glioblastoma (GBM) is among the most aggressive and lethal brain cancers, with a median survival of under 15 months. **MGMT promoter methylation** silences a DNA-repair gene, making tumours more sensitive to **temozolomide (TMZ)** chemotherapy. Methylation status is thus a key predictive biomarker, directly guiding treatment decisions.

MOTIVATION

Determining methylation currently requires surgical biopsy, motivating a non-invasive, imaging-based alternative. Prior work combines 3D MRI with radiomics, but the optimal fusion strategy remains unclear. 3D MRI volumes are computationally expensive and there is limited data, making training from scratch a challenge. We therefore 1) use a pretrained 3D foundation model for feature extraction, and 2) systematically compare fusion strategies for methylation classification.



Dataset: BraTS 2021, 577 GBM patients, four 3D MRI sequences (T1, T1CE, T2, FLAIR).

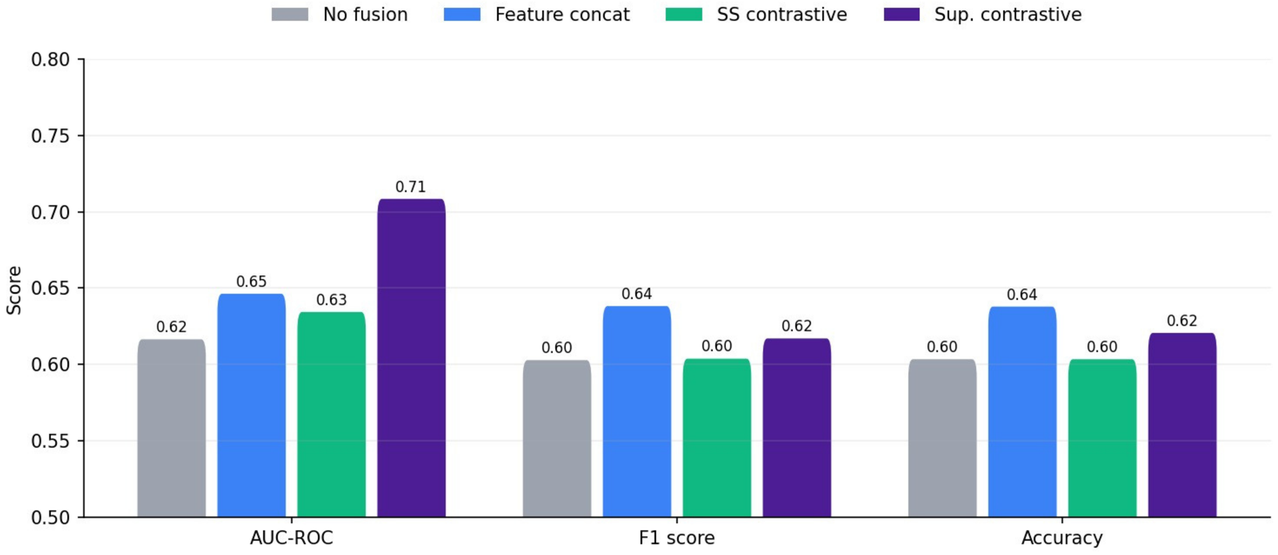
Image Branch: each MRI sequence is encoded by BrainIAC, a pretrained 3D foundation model, then projected to a shared dimension.

Radiomics Branch: features are extracted per sequence x tumour subregion (edema, enhancing tumour, necrotic core) → 12 groups, each passed through an MLP; redundant features are pruned by correlation.

Classification: Binary prediction of MGMT methylation status is performed, which guides treatment planning.

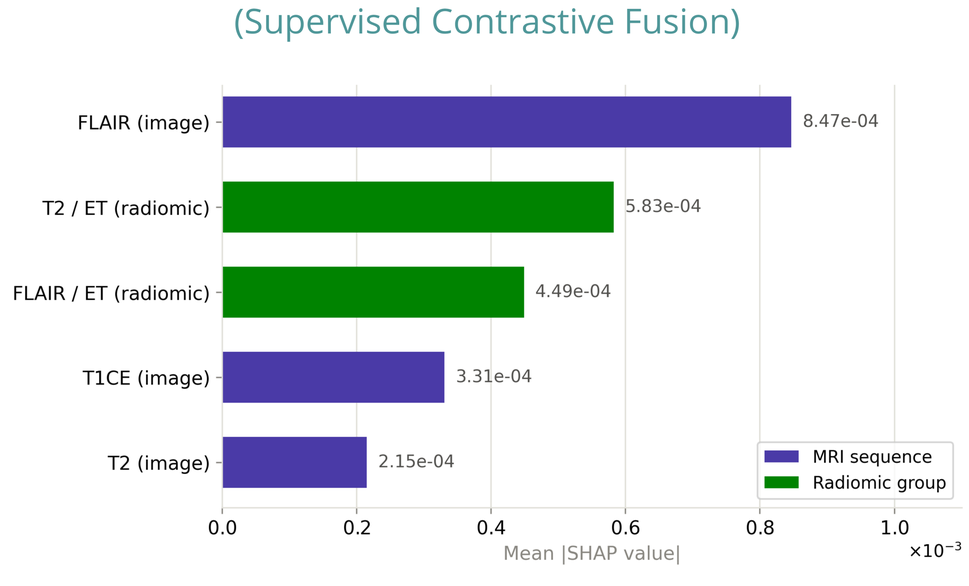
RESULTS

Performance Chart Across All Four Models



Supervised contrastive fusion achieved the highest discriminative performance (AUC-ROC = 0.71), outperforming the no-fusion baseline (0.62), feature concatenation (0.65), and self-supervised contrastive fusion (0.63). F1 and accuracy were comparable across strategies (0.60-0.64), with feature concatenation scoring marginally higher on both. This indicates that class-aware alignment improves separation between methylation classes more than it improves predictions.

SHAP Group-Level Feature Importance (Supervised Contrastive Fusion)



Mean absolute SHAP values were computed for each modality group by aggregating across all dimensions belonging to each MRI sequence or radiomic feature group. Of the 16 modality groups, five showed non-negligible contribution to model predictions: FLAIR image features ranked highest, followed by T2/ET and FLAIR/ET radiomic groups, then T1CE and T2 image features. The remaining groups showed minimal contribution, indicating the model's output is shaped by a narrow set of features rather than drawing evenly from all inputs.

FUTURE WORK

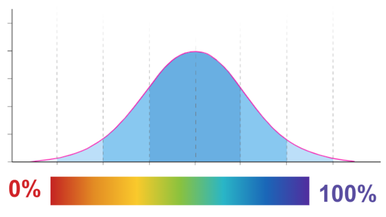
Public Health Scotland Data

~ 2000 GBM patients based in Edinburgh

Treatment and overall survival data over time

Continuous MGMT methylation values

Expanded Patient Cohort: Extend the multimodal fusion pipeline using a Public Health Scotland cohort, incorporating patient demographics, and treatment and overall survival records alongside imaging and radiomics. This will allow the model to leverage a larger sample size and richer information across modalities, improving robustness and generalisability.



Continuous Prediction with Uncertainty Quantification: Move beyond binary methylation classification toward continuous, uncertainty-aware prediction. This will allow the model to express confidence in its predictions, ensuring a more trustworthy decision-support tool that better reflects the underlying tumour biology.

Illustrations created with BioRender.com

References:

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